

**In the Drawings:**

Please replace the drawings of Figures 1A-E (5 sheet) with the corrected drawings of Figures 1A-E submitted herewith (5 sheets).

Please replace the drawings of Figures 25D-I (3 sheets) with the corrected drawings of Figures 25D-I submitted herewith (3 sheets).

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GTCCTTCCACCATGCACTCGCTGGCTTCTGTGGCGTTCTGCTCTGCTCGCCCCGCTG  
 1 CAGGAAGGTGGTACGGTAGGCCAACCGCACAAAGAGACGAGACGAGA -  
     M H S L G F F S V A C S L L A A A -  
  
 CGCTGGCTCCGGGTCCCTCGCCGAGGGCCGGCCGGCCGGCCGGCTTCGAGTCGGACTCG  
 61 GCGACGAGGGCCCAGGGAGCCGCTCCGGCTGGCCGGGGGGGGGGGGGGGGGGGGGG  
     L L P R E A P A A F E S G L D -  
  
 ACCTCTGGACGGGGAGCCCCGACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG  
 121 TGGAGAGCCCTGGCCTCGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGGGGCTGG  
     L S D A E P D A G E A T A Y A S K D L E -  
  
 AGGAGCAGTTACGGTCTGTCCAGTGATGAACTCATGACTGTACTCTACCCAGAAT  
 181 TCCTCTGTCATTGCCAGACACAGGTCACTTACTTGAGTACTGACATGAGATGGGTCTTA  
     E Q L R S V S V D E L M T V L Y P E Y -  
  
 ATTGGAAAATGTACAAGTGTCAAGCTTAAGGAAAGGGGCTGGCAACATAACAGAGAACAGG  
 241 TAACCTTTACATGTTACAGTCGATTCCCTCGACCGGTGTATTGTCTCTGTCC  
     W K M Y K C Q L R K G W Q H N R E Q A -  
  
 CCAACCTCAACTCAAGGACAGAAGGAACTATAAAATTGCTGCAGCACATTATAATACAG

**FIG. 1A**

360  
 +-----+  
 GGTGGAGTTCCCTGTCTGATATTAAACGACGTCGTGTAATAATTATGTC  
 N L N S R T E E T I K F A A H Y N T E -  
 +-----+  
 AGATCTTGAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT  
 361 - +-----+  
 TCTAGAACTTTCATAACTTAACTCACCCTCTTCTGAGTTACGTTACGGTGCCTCCACA  
 I L K S I D N E W R K T Q C M P R E V C -  
 +-----+  
 GTATAGATGTGGGAAGGAGTTGGAGTCGGACAAACACCTTCTTAAACCTCCATGTG  
 421 - +-----+  
 CATATCTACACCCCTTCTCAAACCTCAGCGCTGTTGGAAAGAAATTGGAGGTACAC  
 I D V G K E F G V A T N T F F K P P C V -  
 +-----+  
 TGTCCGGTCTACAGATGTGGGGTTGCTGCAATAAGTGAGGGCTGCAGTGCATGAACACCA  
 481 - +-----+  
 ACAGGGCAGATGTCTACACCCCCAACGACGTTATCACTCCCCGACCGTACGTACTTGTGGT  
 S V Y R C G C C N S E G L Q C M N T S -  
 +-----+  
 GCACGGCTACCTCAGCAAGAGTTATTGAAATTACAGTGCCTCTCTCAAGGGCCCA  
 541 - +-----+  
 CGTGCTGGATGGAGTCCGTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT  
 T S Y L S K T L F E I T V P L S Q G P K -  
 +-----+  
 AACCAAGTAACAAATCAGTTGGCAATCACACTCCTGGGGATGCATGTCATAACTGGATG  
 601 - +-----+  
 TGGTCAATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGATTTGACCTAC  
 P V T I S F A N H T S C R C M S K L D V -

FIG. 1B

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661 TTTACAGACAAGTTCATTCATTAGACCTTCCATTAACTGGCCAGCAACACTACAGTGTC  
 720 AAATGCTGTCAAGGTAAGGTAATAATCTGCAAGGGACGGTCACTGATGGTGTGATGGTGTGTCACAG  
 Y R Q V H S I I R S L P A T L P Q C Q -

AGGCAGGCCAACAGACCTGGCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC  
 780 TCCCGCTGTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACCGTCTACGG  
 A A N K T C P T N Y M W N H I C R C L -

TGGCTCAGGAAAGATTTATGTTTCTCGGATGCTGGAGATGACTCAAACAGATGGATTCC  
 840 ACCGAGTCCTTCTAAATAACAAAAGGAGCCCTACGACCCTACTGAGTTGTCTACCTAACCTAAGG  
 A Q E D F M . F S S D A G D S T D G F H -

ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCACTGTCTGCTGCAGAG  
 900 TACTGTAGACACCTGGTTCTGGACCTACTTCTCTGGACAGTCACACAGACGTCTC  
 D I C G P N K E L D E E T C Q C V C R A -

CGGGGCTTGGGCTTGGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT  
 960 GCCCCGAAAGCCGGACACCTGGTGGTCTTGATCTGTCTTGTGACTACGGTCA  
 G L R P A S C G P H K E L D R N S C Q C -

GTGTCTGTAAAAACAAACTCTTCCAGCCAATGTGGGGCAACCGAGAAATTGATGAAA  
 1020 CACAGACATTTGTGTTGAGAAGGGGTGGTTACACCCGGTCTAAACTACTTT

FIG. 1C

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V C K N K L F P S Q C G A N R E F D E N -  
 ACACATGCCAGTGTATGTAAMAGAACCTGCCAGAAATCAACCCCTAAATCCTGGAA  
 1021 ---+-----+-----+-----+-----+-----+-----+-----+ 1080  
 TGTGTACGGTCACACATACATTCTTGACGGGTCTTAGTTGGGATTAGGACCTT  
 T C Q C V C K R T C P R N Q P L N P G K -

AATGTGCCTGTGAATGTACAGAACAGAACATGCTTGTAAAAGGAAAGAAGTTC  
 1081 ---+-----+-----+-----+-----+-----+-----+-----+ 1140  
 TTACACGGACACTTACATGTCTTCAGGGTCTTACGAAACAATTTCCTTCAAGG  
 C A C E C T E S P Q K C L L K G K F H -

ACCAACCATGGCAGCTGTACAGACGGCCATGTCAGAACCGGCCAGAAGGCTTGTGAGC  
 1141 ---+-----+-----+-----+-----+-----+-----+-----+ 1200  
 TGGTGGTTGTACGTGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCGAACACTCG  
 H Q T C S C Y R R P C T N R Q K A C E P -

CAGGATTTCATATAGTGAAGAACGTTGCTGTCCTTCATATTGGCAAAGACCAC  
 1201 ---+-----+-----+-----+-----+-----+-----+-----+ 1260  
 GTCCCTAAAGTATATCACTTCTCACACAGCAACACAGGAAGTATAACCGTTCTGGTG  
 G F S Y S E E V C R C V P S Y W Q R P Q -

AAATGAGCTAAGATTGTACTGTTCCAGTTCATCGATTCTTATTATGGAAAAACTGTGT

FIG. 1D

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11261 TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAGATAATAACCTTTGACACA  
 M S \* +-----+-----+-----+-----+-----+-----+-----+-----+-----+  
 1321 TGCCACAGTAGAACTTGTCTGTGAACAGAGAACGCCCTTGTGGTCCATGCTAACAAAGACA  
 ACGGTGTCATCTTGACAGACACTTGTCTGGAACACCCCAGGTACGATTGTCTGTCTGT  
 AAAGTCTGTCTTCTGTGAACCATGTGGATAACTTACAGAAATGGACTGGAGCTCATCTG  
 1381 TTTCAAGACAGAAAGGACTTGGTACACCTATTGAATAATGTCTTACCTGACCTCGAGTAGAC  
 CAAAAGGCCCTCTGTAAAGACTGGTTCTGCCAATGACCAAACAGCCAAAGATTTCCTGC  
 GTTTCGGAGAACATTCTGACCAAAAGACGGTTACTGGTTCTAAAPAGGAG  
 1441 TTGTGATTCTTAAAGAATGACTATAATTATTAACTTCCACTAAATAATTGTCTTCTGC  
 AACACTAAAGAAATTCTACTGATATAATTAAATAAGCTGATTTATAACAAAGAGCC  
 1501 ATTCAATTAGCAACACAATTGGTAAACTCACTGTGATCAAATAATTATATCAT  
 TAAGTAAATACTCGTGTGTAACCATTGACTAGTTGACACTAGTTATAAAATATAGTA  
 GCAAAATATGTTAAATAAAATGAAATATTGTATTATAAAATAAAATAAAATAAA  
 CGTTTTATAACAAATTCTTACTTTAACATAAAATTTTGTGTTTTTTTTTTTT  
 1561 1620 1674 1621

FIG. 1

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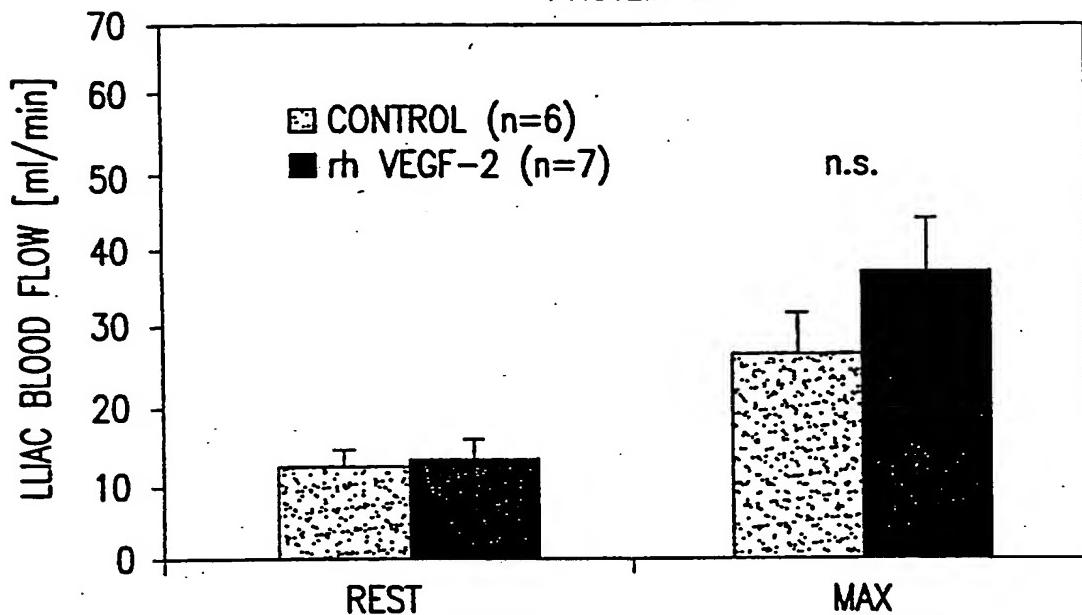
I LIAC BLOOD FLOW  
-PROTEIN I.A.-

FIG.25D

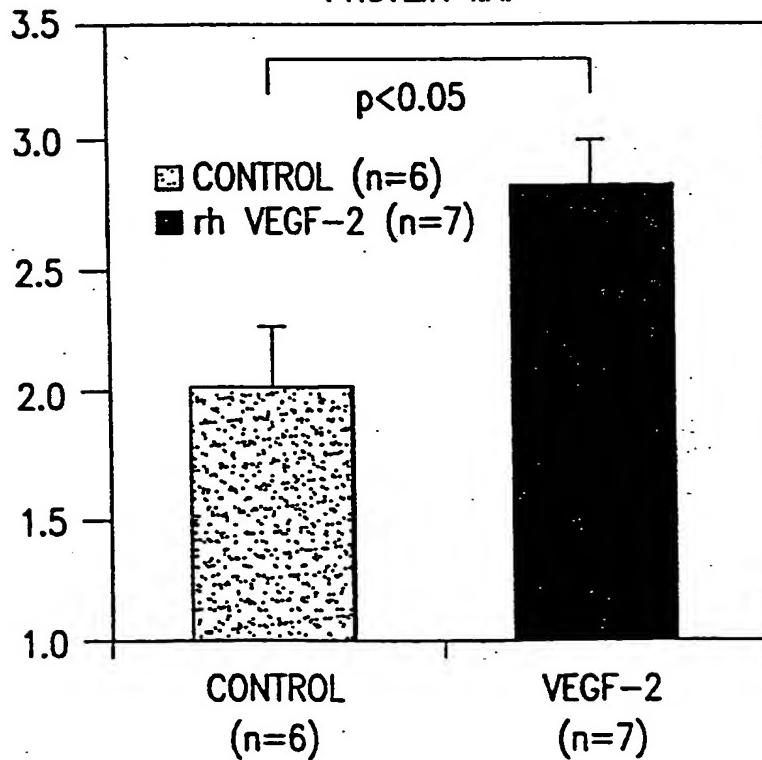
I LIAC FLOW RESERVE  
-PROTEIN I.A.-

FIG.25E

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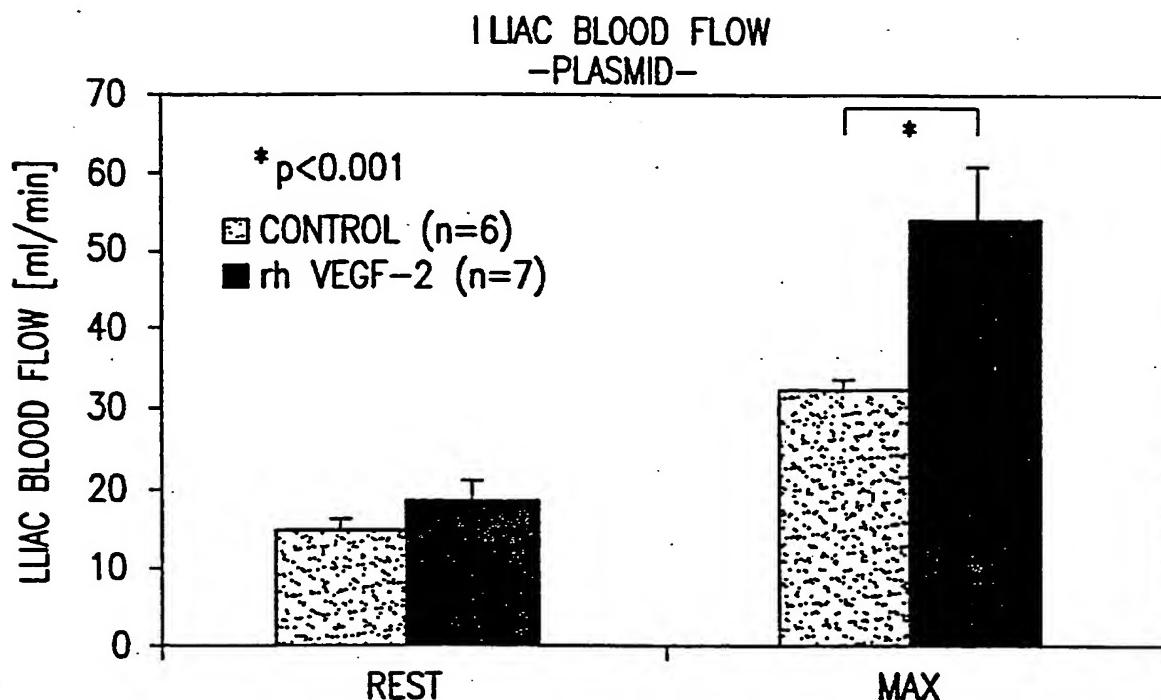


FIG.25F

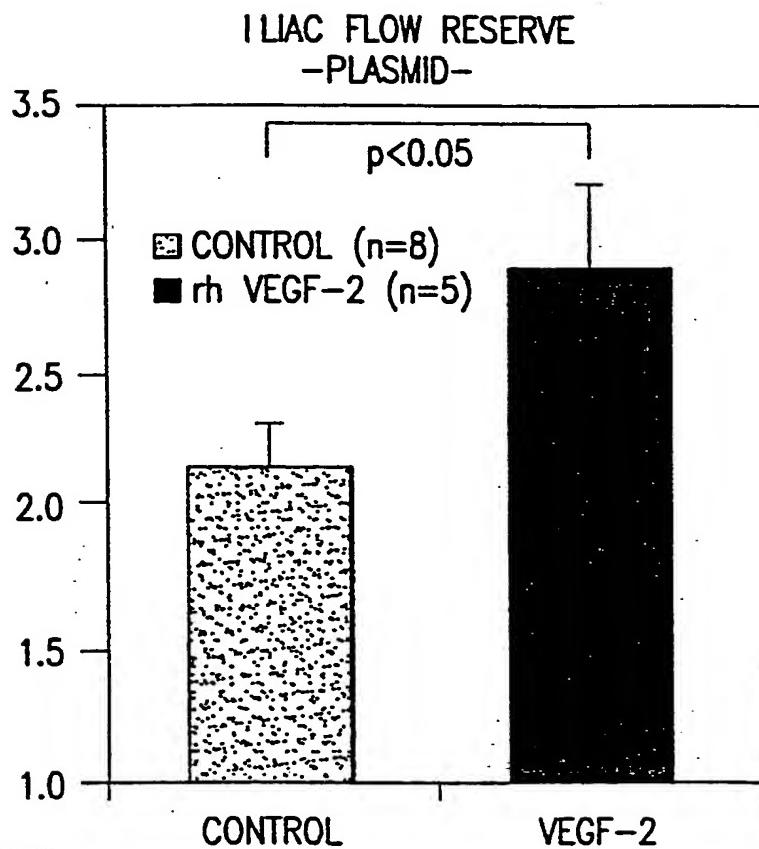


FIG.25G

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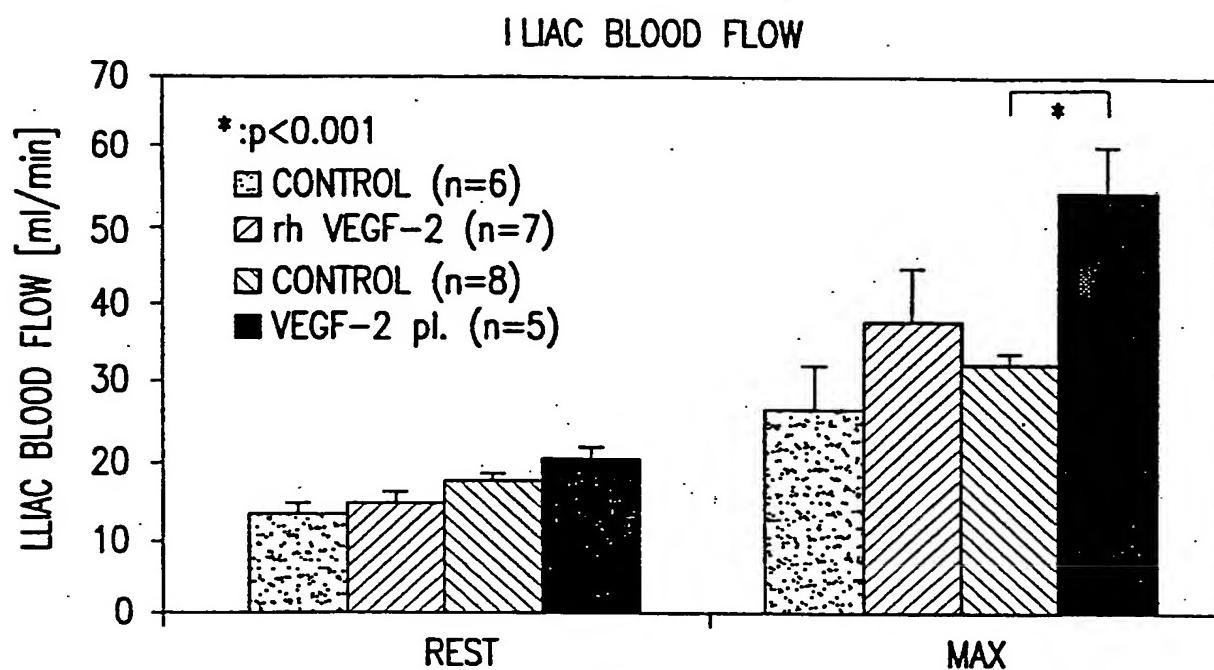


FIG.25H

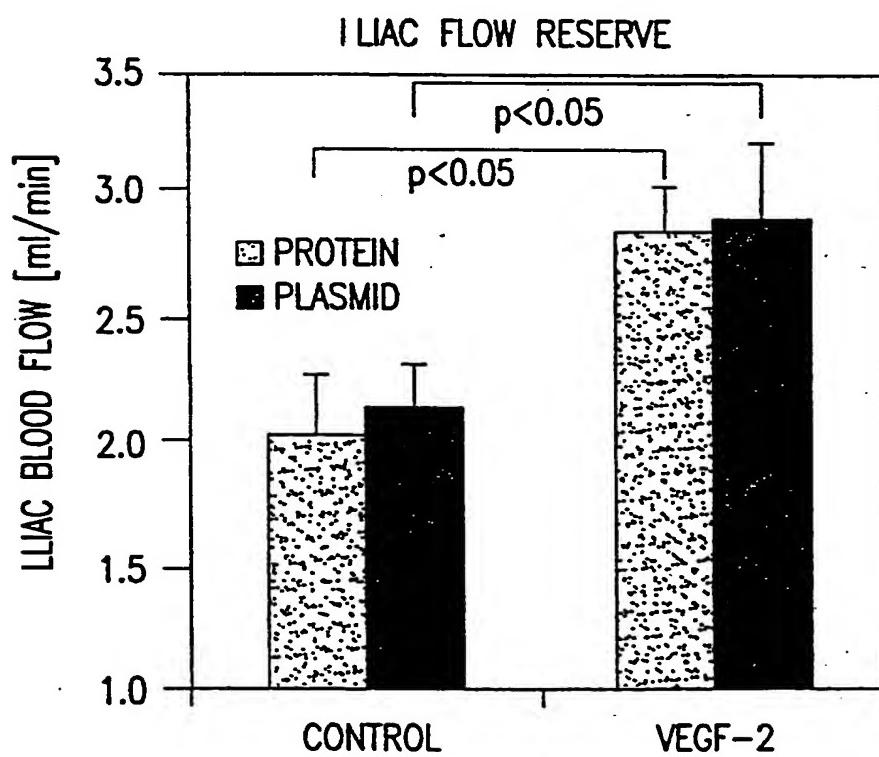


FIG.25I  
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